

TITLE

PLANT AMINOACYL-tRNA SYNTHETASE

ABSTRACT OF THE DISCLOSURE

This invention relates to an isolated nucleic acid fragment encoding an aminoacyl-tRNA synthetase. The invention also relates to the construction of a chimeric gene encoding all or a portion of the aminoacyl-tRNA synthetase, in sense or antisense orientation, wherein expression of the chimeric gene results in production of altered levels of the aminoacyl-tRNA synthetase in a transformed host cell.

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UNITED STATES PATENT AND TRADEMARK OFFICE  
DOCUMENT CLASSIFICATION BARCODE SHEET



# Sequence Listing

9

Level - 2  
Version 1.1

# SEQUENCE LISTING

<110> Falco, S. Carl  
Famodu, Layo O.  
Orozco, Buddy  
Schwaber, James S.

<120> Plant Aminoacyl-tRNA Synthetase

<130> BB-1193

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<150> 60/093,530

<151> July 21, 1998

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 Leu Pro Leu Tyr Tyr Ser Ser Arg Pro His Arg Arg Leu Leu Ala Arg  
 35 40 45  
 Phe Phe Ser Val Ala Ser Ala Pro Gly Gly Ala Lys Gly His Arg Pro  
 50 55 60

Ala Ala Ser Ala Val Glu Val Gly Gly Val Lys Ile Ala Arg Glu Asp  
65 70 75 80

Val Val Lys Glu Asp Asp Pro Thr Asn Asn Val Pro Asp Asn Ile Phe  
85 90 95

Ser Lys Ile Gly Leu Gln Leu His Arg Arg Asp Asn His Pro Leu Gly  
100 105 110

Ile Leu Lys Asn Thr Ile Tyr Asp Tyr Phe Asp Lys Asn Phe Thr Gly  
115 120 125

Gln Phe Asp Lys Phe Asp Asp Leu Cys Pro Leu Val Ser Val Lys Gln  
130 135 140

Asn Phe Asp Asp Val Leu Val Pro Ser Asp His Val Ser Arg Ser Tyr  
145 150 155 160

Asn Asp Thr Tyr Tyr Val Asp Gly Gln Thr Val Leu Arg Cys His Thr  
165 170 175

Ser Ala His Gln Ala Glu Leu Leu Arg His Gly His Thr His Phe Leu  
180 185 190

Val Thr Gly Asp Val Tyr Arg Arg Asp Ser Ile Asp Ser Thr His Tyr  
195 200 205

Pro Val Phe His Gln Met Glu Gly Phe Arg Val Phe Ser Pro Asp Glu  
210 215 220

Trp Ser Gly Ser Arg Met Gly Gly Thr Ala Tyr Ala Ala Ala Glu Leu  
225 230 235 240

Lys Lys Thr Leu Glu Gly Leu Ala Arg His Leu Phe Gly Ala Val Glu  
245 250 255

Met Arg Trp Val Asp Thr Tyr Phe Pro Phe Thr Asn Pro Ser Phe Glu  
260 265 270

Leu Glu Ile Tyr Phe Gln Asp Asp Trp Leu Glu Val Leu Gly Cys Gly  
275 280 285

Val Thr Glu Gln Glu Ile Leu Lys Arg Asn Gly Arg Arg Asp His Val  
290 295 300

Ala Trp Ala Phe Gly Leu Gly Leu Glu Arg Leu Ala Met Val Leu Phe  
305 310 315 320

Asp Ile Pro Asp Ile Arg Leu Phe Trp Ser Asn Asp Lys Arg Phe Thr  
325 330 335

Ser Gln Phe Ser Glu Gly Lys Leu Gly Val Lys Phe Lys Pro Phe Ser  
340 345 350

Lys Phe Pro Pro Cys Tyr Lys Asp Met Ser Phe Trp Ile Asn Asp Ala  
355 360 365

Phe Thr Glu Asn Asn Leu Cys Glu Val Val Arg Gly Ile Ala Gly Asp  
370 375 380



Leu Val Glu Glu Val Lys Leu Ile Asp Asn Phe Thr Asn Lys Lys Gly  
385 390 395 400

Met Thr Ser His Cys Tyr Arg Ile Ala Tyr Arg Ser Met Glu Arg Ser  
405 410 415

Leu Thr Asp Glu Glu Ile Asn Asn Leu Gln Leu Asn Val Arg Glu Ala  
420 425 430

Val Lys Asp Lys Leu Glu Val Glu Leu Arg  
435 440

<210> 19  
<211> 1000  
<212> DNA  
<213> Oryza sativa

<400> 19  
gcacgagtgg taccaacagc atcctgctcg ggattcacac gatacatTTT ttcttgaagc 60  
ccctgccgct acaaaacaat tgcctgaaga ttatcttgag aaagtaaagg aagttcatca 120  
acgtggtggt tatggtctca agggatatgg ctatgactgg aaacgggatg aagcagagaa 180  
aaacctgctt cgtaccaca ctacagcagt ttcaacaagg atgctataca agctagcaca 240  
agagaaacct tttgccccta agaggtacta ctccattgat cgtgttttcc gcaatgaagc 300  
tgtggaccgg actcatcttg cggaattcca ccagattgaa ggtctcattt gtgattatgg 360  
tttgacgctg ggtgatctga ttggtgtatt ggaggatttc ttctcgagtc taggcatgtc 420  
aaagctgcgt ttcaagcctg cctacaatcc atacaccgag ccgagcatgg aaattttcag 480  
ttaccatgaa ggtttgaaga aatgggtgga agttggtaac tctggcatgt tcagacctga 540  
aatgttactt cccatgggac tgccagaggg tggttaatgtt attgcatggg gtctttcact 600  
agaaaggcca acaatgattc ttacggcat cgacaacatt cgagacctct ttggacaaaa 660  
ggttgatttc aacctcatca agagcaaccc tctctgccgc ttgggactgc agtaaaacct 720  
tgcaaaagtt ggttggaagt gattaagtaa caagatttgt ttagttgatc agtggttgaa 780  
cgtgaagaga tcatttctgg cttaccttga aacaccaata catgtgcatt tagcagaggt 840  
ttttgtatta cagttttgag tgatatgaga ctaccagcca atttttgtgt gtgtccatat 900  
tcgaataactt tgatacatTTT taattgagca catccaatgt atgaagtggg catctgccgc 960  
tgcggttgct tgaatcaaaa aaaaaaaaaa aaaaaaaaaa 1000

<210> 20  
<211> 237  
<212> PRT  
<213> Oryza sativa

<400> 20  
His Glu Trp Tyr Gln Gln His Pro Ala Arg Asp Ser His Asp Thr Phe  
1 5 10 15  
Phe Leu Glu Ala Pro Ala Ala Thr Lys Gln Leu Pro Glu Asp Tyr Leu  
20 25 30  
Glu Lys Val Lys Glu Val His Gln Arg Gly Gly Tyr Gly Ser Lys Gly  
35 40 45  
Tyr Gly Tyr Asp Trp Lys Arg Asp Glu Ala Glu Lys Asn Leu Leu Arg  
50 55 60  
Thr His Thr Thr Ala Val Ser Thr Arg Met Leu Tyr Lys Leu Ala Gln  
65 70 75 80  
Glu Lys Pro Phe Ala Pro Lys Arg Tyr Tyr Ser Ile Asp Arg Val Phe  
85 90 95

TC4253 "4344360

Arg Asn Glu Ala Val Asp Arg Thr His Leu Ala Glu Phe His Gln Ile  
100 105 110

Glu Gly Leu Ile Cys Asp Tyr Gly Leu Thr Leu Gly Asp Leu Ile Gly  
115 120 125

Val Leu Glu Asp Phe Phe Ser Ser Leu Gly Met Ser Lys Leu Arg Phe  
130 135 140

Lys Pro Ala Tyr Asn Pro Tyr Thr Glu Pro Ser Met Glu Ile Phe Ser  
145 150 155 160

Tyr His Glu Gly Leu Lys Lys Trp Val Glu Val Gly Asn Ser Gly Met  
165 170 175

Phe Arg Pro Glu Met Leu Leu Pro Met Gly Leu Pro Glu Gly Val Asn  
180 185 190

Val Ile Ala Trp Gly Leu Ser Leu Glu Arg Pro Thr Met Ile Leu Tyr  
195 200 205

Gly Ile Asp Asn Ile Arg Asp Leu Phe Gly Pro Lys Val Asp Phe Asn  
210 215 220

Leu Ile Lys Ser Asn Pro Leu Cys Arg Leu Gly Leu Gln  
225 230 235

<210> 21  
<211> 387  
<212> DNA  
<213> Glycine max

<220>  
<221> unsure  
<222> (337)

<220>  
<221> unsure  
<222> (379)

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catgggtgtc cctccaaatg gtggccatct tcacacttta cttaaattgca gaactatgat 120  
gaaagaaatc ttcttggaat tgggatttga agaaatgcca accaacaatt acgttgaatc 180  
ttctttcttg aattttgata ctttatttca acctcaacaa catcctgctc gtgatgctca 240  
cgatactttc ttccctttctg aacctgcatc tgccaaatcc attccacaag attattttaga 300  
aagagtgaaa acaatgcatg agaaaaggagg gcacggntct attggttgga gatacgactg 360  
gagtggaaac tgagtccana aaaaaaaa 387

<210> 22  
<211> 123  
<212> PRT  
<213> Glycine max

<400> 22  
Ile Ala Asn Gly Ser Trp Lys Glu Lys Ser Phe Lys Ser Leu Asn Leu  
1 5 10 15

Gly Lys Gly Val Met Gly Val Pro Pro Asn Gly Gly His Leu His Thr  
20 25 30

Leu Leu Lys Cys Arg Thr Met Met Lys Glu Ile Phe Leu Glu Met Gly  
 35 40 45  
 Phe Glu Glu Met Pro Thr Asn Asn Tyr Val Glu Ser Ser Phe Trp Asn  
 50 55 60  
 Phe Asp Thr Leu Phe Gln Pro Gln Gln His Pro Ala Arg Asp Ala His  
 65 70 75 80  
 Asp Thr Phe Phe Leu Ser Glu Pro Ala Ser Ala Lys Ser Ile Pro Gln  
 85 90 95  
 Asp Tyr Leu Glu Arg Val Lys Thr Met His Glu Lys Gly Gly His Gly  
 100 105 110  
 Ser Ile Gly Trp Arg Tyr Asp Trp Ser Gly Asn  
 115 120

<210> 23  
 <211> 1074  
 <212> DNA  
 <213> Triticum aestivum

<400> 23  
 gcacgagggg caacctattg cgataggata tagccaaccg ttgttagagg tccgtgaggc 60  
 aatccagaac atttttctcg agatgggggt cagtgagatg ccaacgaaca tgtatgtaga 120  
 gagcagcttc tgggaatttt atgcactggt ccagccacaa cagcatcctg ctctgtgattc 180  
 acacgatacc tttttcctca aagcccctgc tacaacaaca caattacctg atgactatct 240  
 tgagaaagta aagcaagtac atcagtctgg tggatcatgg tccaaaggat atggttacga 300  
 ttggaagcga gatgaagcag agaaaaacct gcttcgtact cacacaactg cagtttcaac 360  
 aaggatgcta tacaagctag cacaggagaa aacttttgct cctaagagat actattctat 420  
 tgatcgtggt ttccggaatg aagctgtgga ccgaactcat cttgcagaat tccaccagat 480  
 agaaggtcct atttgtgatt atggtttgac gcttggtgat ctgatagggt tattggagga 540  
 tttcttctcc agactaggca tgtcaaagct gcgtttcaaa cctgcctaca acccggtacac 600  
 tgaaccaagc atggaaattt tcagctacca cgatggtctg aagaaatggg tggaaatagg 660  
 caactcaggc atgttcaggc cggaaatggt acttcccatg ggactgccag aggggtgttaa 720  
 tgttatcgca tgggggtctt cgcttgaaag gccacaatg attctgtatg ggattgacaa 780  
 catacgtgat ctctttgggc caaaggtcga cttcaatctg atcaagagca gcccgatttg 840  
 ccgcttgggg ctgtagtggt gtgagcttga tagaacttta tctggatgtc tggatgcgaa 900  
 ggatgtttat ttgtggttat acctttgaaa accagtactt gtgcatttaa cagagggagt 960  
 gcagaaatac acacatgtag ctctgaattg caaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020  
 aataaaaaaa aaacaaaaaa aaaaaaaaaa tactcgaggg ggggccgtac caca 1074

<210> 24  
 <211> 284  
 <212> PRT  
 <213> Triticum aestivum

<400> 24  
 His Glu Gly Gln Pro Ile Ala Ile Gly Tyr Ser Gln Pro Leu Leu Glu  
 1 5 10 15  
 Val Arg Glu Ala Ile Gln Asn Ile Phe Leu Glu Met Gly Phe Ser Glu  
 20 25 30  
 Met Pro Thr Asn Met Tyr Val Glu Ser Ser Phe Trp Asn Phe Asp Ala  
 35 40 45

Leu Phe Gln Pro Gln Gln His Pro Ala Arg Asp Ser His Asp Thr Phe  
50 55 60

Phe Leu Lys Ala Pro Ala Thr Thr Thr Gln Leu Pro Asp Asp Tyr Leu  
65 70 75 80

Glu Lys Val Lys Gln Val His Gln Ser Gly Gly His Gly Ser Lys Gly  
85 90 95

Tyr Gly Tyr Asp Trp Lys Arg Asp Glu Ala Glu Lys Asn Leu Leu Arg  
100 105 110

Thr His Thr Thr Ala Val Ser Thr Arg Met Leu Tyr Lys Leu Ala Gln  
115 120 125

Glu Lys Thr Phe Ala Pro Lys Arg Tyr Tyr Ser Ile Asp Arg Val Phe  
130 135 140

Arg Asn Glu Ala Val Asp Arg Thr His Leu Ala Glu Phe His Gln Ile  
145 150 155 160

Glu Gly Leu Ile Cys Asp Tyr Gly Leu Thr Leu Gly Asp Leu Ile Gly  
165 170 175

Val Leu Glu Asp Phe Phe Ser Arg Leu Gly Met Ser Lys Leu Arg Phe  
180 185 190

Lys Pro Ala Tyr Asn Pro Tyr Thr Glu Pro Ser Met Glu Ile Phe Ser  
195 200 205

Tyr His Asp Gly Leu Lys Lys Trp Val Glu Ile Gly Asn Ser Gly Met  
210 215 220

Phe Arg Pro Glu Met Leu Leu Pro Met Gly Leu Pro Glu Gly Val Asn  
225 230 235 240

Val Ile Ala Trp Gly Leu Ser Leu Glu Arg Pro Thr Met Ile Leu Tyr  
245 250 255

Gly Ile Asp Asn Ile Arg Asp Leu Phe Gly Pro Lys Val Asp Phe Asn  
260 265 270

Leu Ile Lys Ser Ser Pro Ile Cys Arg Leu Gly Leu  
275 280

<210> 25  
<211> 1939  
<212> DNA  
<213> Zea mays

<400> 25  
gtccggaatt cccgggtcga cccacgcgtc cgtgctgtcc cattggcaac ttgcgcgcta 60  
ctctgactcg agtggccgct actctacccc acccacaccc ttccgcccgc cgccactaaa 120  
ccctagcggg acaccgcct tgctcgcgcc gcctcatcct ctactcctc tcggaccccc 180  
ggtggccggt gcagagctgc gcgaccgaga accgaatctg tgagccatgt cgaccaacaa 240  
gggcagcgcg gccaaagggcg gcggagggaa gaagaaggag gtgaagaagg agacgaagct 300  
cgggatggcc tataagaagg acgacaactt cggggagtgg tactccgagg ttgttggttaa 360  
cagtgaatg attgagtact atgacatttc tggttgttat atattgaggc catgggcgat 420  
ggaaatctgg gagctactga aagaattctt tgatgcagaa attaaaaagc tgaagctcaa 480  
accatattat ttccctttgt ttgttactga gaatgttcta cagaaggaaa aggaccacat 540

<210>	26
<211>	383
<212>	PRT
<213>	Zea mays

<400>																26
Pro	Ile	Ala	Ile	Arg	Pro	Thr	Ser	Glu	Thr	Val	Met	Tyr	Pro	Tyr	Phe	
1				5					10					15		
Ser	Lys	Trp	Ile	Arg	Ser	His	Arg	Asp	Leu	Pro	Leu	Arg	Cys	Asn	Gln	
			20					25					30			
Trp	Cys	Asn	Val	Val	Arg	Trp	Glu	Phe	Ser	Asn	Pro	Thr	Pro	Phe	Ile	
		35					40					45				
Arg	Ser	Arg	Glu	Phe	Leu	Trp	Gln	Glu	Gly	His	Thr	Ala	Phe	Ala	Thr	
	50					55					60					
Lys	Glu	Glu	Ala	Asp	Glu	Glu	Val	Leu	Gln	Ile	Leu	Glu	Leu	Tyr	Arg	
65					70					75					80	
Arg	Ile	Tyr	Glu	Glu	Phe	Leu	Ala	Val	Pro	Val	Ser	Lys	Gly	Arg	Lys	
				85					90					95		
Ser	Glu	Met	Glu	Lys	Phe	Ala	Gly	Gly	Leu	Tyr	Thr	Thr	Ser	Val	Glu	
			100					105					110			
Ala	Phe	Ile	Pro	Asn	Thr	Gly	Arg	Gly	Ile	Gln	Gly	Ala	Thr	Ser	His	
		115					120					125				
Cys	Leu	Gly	Gln	Asn	Phe	Ala	Lys	Met	Phe	Asp	Ile	Thr	Phe	Glu	Asn	
	130					135					140					
Glu	Lys	Gly	Val	Arg	Glu	Met	Val	Trp	Gln	Asn	Ser	Trp	Ala	Tyr	Thr	
145					150					155					160	

Thr	Arg	Ser	Ile	Gly	Val	Met	Val	Met	Thr	His	Gly	Asp	Asp	Lys	Gly	165	170	175
Leu	Val	Leu	Pro	Pro	Lys	Val	Ala	Pro	Ile	Gln	Val	Ile	Val	Ile	Ser	180	185	190
Val	Pro	Tyr	Lys	Asp	Ala	Asp	Thr	Thr	Ala	Ile	Lys	Gly	Ala	Cys	Glu	195	200	205
Ser	Thr	Val	Tyr	Thr	Leu	Asp	Gln	Ser	Gly	Ile	Arg	Ala	Asp	Gln	Asp	210	215	220
Thr	Arg	Glu	Asn	Tyr	Ser	Pro	Gly	Trp	Lys	Tyr	Ser	His	Trp	Glu	Met	225	230	235
Lys	Gly	Val	Pro	Leu	Arg	Ile	Glu	Ile	Gly	Pro	Lys	Asp	Leu	Ala	Asn	245	250	255
Lys	Gln	Val	Arg	Val	Val	Arg	Arg	Asp	Asn	Gly	Ala	Lys	Val	Asp	Ile	260	265	270
Pro	Val	Thr	Asn	Leu	Val	Glu	Glu	Val	Lys	Val	Leu	Leu	Asp	Glu	Ile	275	280	285
Gln	Lys	Asn	Leu	Phe	Lys	Thr	Ala	Gln	Glu	Lys	Arg	Asp	Ala	Cys	Val	290	295	300
His	Val	Val	Asn	Thr	Trp	Asp	Glu	Phe	Thr	Thr	Ala	Leu	Asn	Asn	Lys	305	310	315
Lys	Leu	Ile	Leu	Ala	Pro	Trp	Cys	Asp	Glu	Glu	Glu	Ile	Glu	Lys	Asp	325	330	335
Val	Lys	Thr	Arg	Thr	Lys	Gly	Glu	Leu	Gly	Ala	Ala	Lys	Thr	Leu	Cys	340	345	350
Thr	Pro	Phe	Glu	Gln	Pro	Glu	Leu	Pro	Glu	Gly	Thr	Leu	Cys	Phe	Ala	355	360	365
Ser	Gly	Lys	Pro	Ala	Lys	Lys	Trp	Ser	Phe	Trp	Gly	Arg	Ser	Tyr		370	375	380

<210> 27  
 <211> 697  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> unsure  
 <222> (11)

<220>  
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 <222> (40)

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<220>  
<221> unsure  
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<222> (304)

<220>  
<221> unsure  
<222> (503)

<220>  
<221> unsure  
<222> (632)

<220>  
<221> unsure  
<222> (694)

<400> 27  
gtgaaacagt natgtatccc tactactcta agtggataan gngacatcgt gacttgcctt 60  
tgaaacttaa tcagtgggtgc aatgtttgtaa natgggagtt cagcaacccc actccatnca 120  
tcaggagtcg cgagtttctt tggcaagaag ggcacactgc ttttgcaaca aaggatgaag 180  
canatgcaga agttcttgag attctggaat tatataggcg tatatacgaa gagtatttgg 240  
cagttcctgt cataaagggt aagaanagtg agcttgagaa gtttgctggg ggactctaca 300  
ctancaatgt tgaggcattt attccaaaca ctggctcgtgg tatccaagggt gcaacttctc 360  
attgtttggg ccaaaatttt gctaaaatgt ttgagataaa ctttgaaaat gaaaagggag 420  
agaaagcaat ggtctggcag aattcatggg cctatagtag tcgaactatt ggggtcatgg 480  
tgatggttca tgggtgatgac aangggattg gtactacctc cttaaagtagc atcagtacaa 540  
gttattgtga ttctgtgcc ttacaaagat gccgatactc aaggaatctt tgatgcctgt 600  
ctgcactgtg aatacattga tgaagcagga tngcgtgag cagatctaga gatatatctc 660  
ctggatgaga tccactggga atgaaagggt ctcnaga 697

<210> 28  
<211> 173  
<212> PRT  
<213> Glycine max

<220>  
<221> UNSURE  
<222> (13)..(14)

<220>  
<221> UNSURE  
<222> (30)

<220>  
 <221> UNSURE  
 <222> (39)

<220>  
 <221> UNSURE  
 <222> (61)

<220>  
 <221> UNSURE  
 <222> (88)

<220>  
 <221> UNSURE  
 <222> (101)

<220>  
 <221> UNSURE  
 <222> (167)

<400> 28  
 Glu Thr Val Met Tyr Pro Tyr Tyr Ser Lys Trp Ile Xaa Xaa His Arg  
   1                  5                  10                  15  
 Asp Leu Pro Leu Lys Leu Asn Gln Trp Cys Asn Val Val Xaa Trp Glu  
           20                  25                  30  
 Phe Ser Asn Pro Thr Pro Xaa Ile Arg Ser Arg Glu Phe Leu Trp Gln  
           35                  40                  45  
 Glu Gly His Thr Ala Phe Ala Thr Lys Asp Glu Ala Xaa Ala Glu Val  
   50                  55                  60  
 Leu Glu Ile Leu Glu Leu Tyr Arg Arg Ile Tyr Glu Glu Tyr Leu Ala  
   65                  70                  75                  80  
 Val Pro Val Ile Lys Gly Lys Xaa Ser Glu Leu Glu Lys Phe Ala Gly  
           85                  90                  95  
 Gly Leu Tyr Thr Xaa Asn Val Glu Ala Phe Ile Pro Asn Thr Gly Arg  
           100                  105                  110  
 Gly Ile Gln Gly Ala Thr Ser His Cys Leu Gly Gln Asn Phe Ala Lys  
           115                  120                  125  
 Met Phe Glu Ile Asn Phe Glu Asn Glu Lys Gly Glu Lys Ala Met Val  
   130                  135                  140  
 Trp Gln Asn Ser Trp Ala Tyr Ser Thr Arg Thr Ile Gly Val Met Val  
   145                  150                  155                  160  
 Met Val His Gly Asp Asp Xaa Gly Ile Gly Thr Thr Ser  
           165                  170

<210> 29  
 <211> 564  
 <212> DNA  
 <213> Triticum aestivum



<220>  
 <221> unsure  
 <222> (439)

<220>  
 <221> unsure  
 <222> (466)

<220>  
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 <222> (526)

<220>  
 <221> unsure  
 <222> (536)

<220>  
 <221> unsure  
 <222> (564)

<400> 29  
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 ttttgcaact aaagaggagg cagatgaaga ggtcctccaa atattggaac totacaggag 120  
 aatatatgaa gaatttttag cagttccagt gtccaaaggg aggaaaagtg agatggaaaa 180  
 gtttgctggt ggactttata caaccagtgt agaggccttc attccaaata ctggccgtgg 240  
 tatacaagggt gcaacttcac attgtcttgg tcaaaaacttt gcaaagatgt ttgatatacac 300  
 tttcgagaat gaaaagggtg aacgggtccat ggtgtggcag aactottggg catacactac 360  
 ccgctcgatt ggggtcatga taatgacaca tggatgatgac aagggttag tgctgccacc 420  
 aaagggtgacc tatccaggnc attgtatcct gtgccattaa agatgntgac acaacagcta 480  
 ttaaaggggc gtcgagcggc gttacacctt gaccaactgg atcggnagat ttgatnccgt 540  
 gaaatacccc cagggtggaaa atcn 564

<210> 30  
 <211> 152  
 <212> PRT  
 <213> Triticum aestivum

<400> 30  
 Ser Asn Pro Thr Pro Phe Ile Arg Ser Arg Glu Phe Leu Trp Gln Glu  
 1 5 10 15  
 Gly His Thr Val Phe Ala Thr Lys Glu Glu Ala Asp Glu Glu Val Leu  
 20 25 30  
 Gln Ile Leu Glu Leu Tyr Arg Arg Ile Tyr Glu Glu Phe Leu Ala Val  
 35 40 45  
 Pro Val Ser Lys Gly Arg Lys Ser Glu Met Glu Lys Phe Ala Gly Gly  
 50 55 60  
 Leu Tyr Thr Thr Ser Val Glu Ala Phe Ile Pro Asn Thr Gly Arg Gly  
 65 70 75 80  
 Ile Gln Gly Ala Thr Ser His Cys Leu Gly Gln Asn Phe Ala Lys Met  
 85 90 95  
 Phe Asp Ile Thr Phe Glu Asn Glu Lys Gly Glu Arg Ser Met Val Trp  
 100 105 110

Gln Asn Ser Trp Ala Tyr Thr Thr Arg Ser Ile Gly Val Met Ile Met  
115 120 125

Thr His Gly Asp Asp Lys Gly Leu Val Leu Pro Pro Lys Val Thr Tyr  
130 135 140

Pro Gly His Cys Ile Leu Cys His  
145 150

<210> 31  
<211> 1072  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 31  
Met Ser Glu Ser Asn Ala His Phe Ser Phe Pro Lys Glu Glu Glu Lys  
1 5 10 15

Val Leu Ser Leu Trp Asp Glu Ile Asp Ala Phe His Thr Ser Leu Glu  
20 25 30

Leu Thr Lys Asp Lys Pro Glu Phe Ser Phe Phe Asp Gly Pro Pro Phe  
35 40 45

Ala Thr Gly Thr Pro His Tyr Gly His Ile Leu Ala Ser Thr Ile Lys  
50 55 60

Asp Ile Val Pro Arg Tyr Ala Thr Met Thr Gly His His Val Glu Arg  
65 70 75 80

Arg Phe Gly Trp Asp Thr His Gly Val Pro Ile Glu His Ile Ile Asp  
85 90 95

Lys Lys Leu Gly Ile Thr Gly Lys Asp Asp Val Phe Lys Tyr Gly Leu  
100 105 110

Glu Asn Tyr Asn Asn Glu Cys Arg Ser Ile Val Met Thr Tyr Ala Ser  
115 120 125

Asp Trp Arg Lys Thr Ile Gly Arg Leu Gly Arg Trp Ile Asp Phe Asp  
130 135 140

Asn Asp Tyr Lys Thr Met Tyr Pro Ser Phe Met Glu Ser Thr Trp Trp  
145 150 155 160

Ala Phe Lys Gln Leu His Glu Lys Gly Gln Val Tyr Arg Gly Phe Lys  
165 170 175

Val Met Pro Tyr Ser Thr Gly Leu Thr Thr Pro Leu Ser Asn Phe Glu  
180 185 190

Ala Gln Gln Asn Tyr Lys Asp Val Asn Asp Pro Ala Val Thr Ile Gly  
195 200 205

Phe Asn Val Ile Gly Gln Glu Lys Thr Gln Leu Val Ala Trp Thr Thr  
210 215 220

Thr Pro Trp Thr Leu Pro Ser Asn Leu Ser Leu Cys Val Asn Ala Asp  
225 230 235 240



Glu	Gly	Leu	Asp	Gln	Thr	Arg	Gly	Trp	Phe	Tyr	Thr	Leu	Ala	Val	Leu	
				565					570					575		
Gly	Thr	His	Leu	Phe	Gly	Ser	Val	Pro	Tyr	Lys	Asn	Val	Ile	Val	Ser	
			580					585					590			
Gly	Ile	Val	Leu	Ala	Ala	Asp	Gly	Arg	Lys	Met	Ser	Lys	Ser	Leu	Lys	
		595					600					605				
Asn	Tyr	Pro	Asp	Pro	Ser	Ile	Val	Leu	Asn	Lys	Tyr	Gly	Ala	Asp	Ala	
	610					615					620					
Leu	Arg	Leu	Tyr	Leu	Ile	Asn	Ser	Pro	Val	Leu	Lys	Ala	Glu	Ser	Leu	
625					630					635					640	
Lys	Phe	Lys	Glu	Glu	Gly	Val	Lys	Glu	Val	Val	Ser	Lys	Val	Leu	Leu	
			645					650						655		
Pro	Trp	Trp	Asn	Ser	Phe	Lys	Phe	Leu	Asp	Gly	Gln	Ile	Ala	Leu	Leu	
			660					665					670			
Lys	Lys	Met	Ser	Asn	Ile	Asp	Phe	Gln	Tyr	Asp	Asp	Ser	Val	Lys	Ser	
		675					680					685				
Asp	Asn	Val	Met	Asp	Arg	Trp	Ile	Leu	Ala	Ser	Met	Gln	Ser	Leu	Val	
	690					695					700					
Gln	Phe	Ile	His	Glu	Glu	Met	Gly	Gln	Tyr	Lys	Leu	Tyr	Thr	Val	Val	
705					710					715					720	
Pro	Lys	Leu	Leu	Asn	Phe	Ile	Asp	Glu	Leu	Thr	Asn	Trp	Tyr	Ile	Arg	
				725				730						735		
Phe	Asn	Arg	Arg	Arg	Leu	Lys	Gly	Glu	Asn	Gly	Val	Glu	Asp	Cys	Leu	
			740					745					750			
Lys	Ala	Leu	Asn	Ser	Leu	Phe	Asp	Ala	Leu	Phe	Thr	Phe	Val	Arg	Ala	
	755						760					765				
Met	Ala	Pro	Phe	Thr	Pro	Phe	Leu	Ser	Glu	Ser	Ile	Tyr	Leu	Arg	Leu	
	770					775					780					
Lys	Glu	Tyr	Ile	Pro	Glu	Ala	Val	Leu	Ala	Lys	Tyr	Gly	Lys	Asp	Gly	
785					790					795					800	
Arg	Ser	Val	His	Phe	Leu	Ser	Tyr	Pro	Val	Val	Lys	Lys	Glu	Tyr	Phe	
			805					810						815		
Asp	Glu	Ala	Ile	Glu	Thr	Ala	Val	Ser	Arg	Met	Gln	Ser	Val	Ile	Asp	
			820					825					830			
Leu	Gly	Arg	Asn	Ile	Arg	Glu	Lys	Lys	Thr	Ile	Ser	Leu	Lys	Thr	Pro	
		835					840					845				
Leu	Lys	Thr	Leu	Val	Ile	Leu	His	Ser	Asp	Glu	Ser	Tyr	Leu	Lys	Asp	
	850					855					860					
Val	Glu	Ala	Leu	Lys	Asn	Tyr	Ile	Ile	Glu	Glu	Leu	Asn	Val	Arg	Asp	
865					870					875					880	







Trp Tyr Val Arg Met Asn Arg Arg Arg Leu Lys Gly Glu Asn Gly Met  
740 745 750

Glu Asp Cys Val Met Ala Leu Glu Thr Leu Phe Ser Val Leu Leu Ser  
755 760 765

Leu Cys Arg Leu Met Ala Pro Tyr Thr Pro Phe Leu Thr Glu Leu Met  
770 775 780

Tyr Gln Asn Leu Lys Val Leu Ile Asp Pro Val Ser Val Gln Asp Lys  
785 790 795 800

Asp Thr Leu Ser Ile His Tyr Leu Met Leu Pro Arg Val Arg Glu Glu  
805 810 815

Leu Ile Asp Lys Lys Thr Glu Ser Ala Val Ser Gln Met Gln Ser Val  
820 825 830

Ile Glu Leu Gly Arg Val Ile Arg Asp Arg Lys Thr Ile Pro Ile Lys  
835 840 845

Tyr Pro Leu Lys Glu Ile Val Val Ile His Gln Asp Pro Glu Ala Leu  
850 855 860

Lys Asp Ile Lys Ser Leu Glu Lys Tyr Ile Ile Glu Glu Leu Asn Val  
865 870 875 880

Arg Lys Val Thr Leu Ser Thr Asp Lys Asn Lys Tyr Gly Ile Arg Leu  
885 890 895

Arg Ala Glu Pro Asp His Met Val Leu Gly Lys Arg Leu Lys Gly Ala  
900 905 910

Phe Lys Ala Val Met Thr Ser Ile Lys Gln Leu Ser Ser Glu Glu Leu  
915 920 925

Glu Gln Phe Gln Lys Thr Gly Thr Ile Val Val Glu Gly His Glu Leu  
930 935 940

His Asp Glu Asp Ile Arg Leu Met Tyr Thr Phe Asp Gln Ala Thr Gly  
945 950 955 960

Gly Thr Ala Gln Phe Glu Ala His Ser Asp Ala Gln Ala Leu Val Leu  
965 970 975

Leu Asp Val Thr Pro Asp Gln Ser Met Val Asp Glu Gly Met Ala Arg  
980 985 990

Glu Val Ile Asn Arg Ile Gln Lys Leu Arg Lys Lys Cys Asn Leu Val  
995 1000 1005

Pro Thr Asp Glu Ile Thr Val Tyr Tyr Lys Ala Lys Ser Glu Gly Thr  
1010 1015 1020

Tyr Leu Asn Ser Val Ile Glu Ser His Thr Glu Phe Ile Phe Thr Thr  
1025 1030 1035 1040

Ile Lys Ala Pro Leu Lys Pro Tyr Pro Val Ser Pro Ser Asp Lys Val  
1045 1050 1055



Leu Ile Gln Glu Lys Thr Gln Leu Lys Gly Ser Glu Leu Glu Ile Thr  
1060 1065 1070

Leu Thr Arg Gly Ser Ser Leu Pro Gly Pro Ala Cys Ala Tyr Val Asn  
1075 1080 1085

Leu Asn Ile Cys Ala Asn Gly Ser Glu Gln Gly Gly Val Leu Leu Leu  
1090 1095 1100

Glu Asn Pro Lys Gly Asp Asn Arg Leu Asp Leu Leu Lys Leu Lys Ser  
1105 1110 1115 1120

Val Val Thr Ser Ile Phe Gly Val Lys Asn Thr Glu Leu Ala Val Phe  
1125 1130 1135

His Asp Glu Thr Glu Ile Gln Asn Gln Thr Asp Leu Leu Ser Leu Ser  
1140 1145 1150

Gly Lys Thr Leu Cys Val Thr Ala Gly Ser Ala Pro Ser Leu Ile Asn  
1155 1160 1165

Ser Ser Ser Thr Leu Leu Cys Gln Tyr Ile Asn Leu Gln Leu Leu Asn  
1170 1175 1180

Ala Lys Pro Gln Glu Cys Leu Met Gly Thr Val Gly Thr Leu Leu Leu  
1185 1190 1195 1200

Glu Asn Pro Leu Gly Gln Asn Gly Leu Thr His Gln Gly Leu Leu Tyr  
1205 1210 1215

Glu Ala Ala Lys Val Phe Gly Leu Arg Ser Arg Lys Leu Lys Leu Phe  
1220 1225 1230

Leu Asn Glu Thr Gln Thr Gln Glu Ile Thr Glu Asp Ile Pro Val Lys  
1235 1240 1245

Thr Leu Asn Met Lys Thr Val Tyr Val Ser Val Leu Pro Thr Thr Ala  
1250 1255 1260

Asp Phe  
1265

<210> 33  
<211> 1262  
<212> PRT  
<213> Homo sapiens

<400> 33  
Met Leu Gln Gln Val Pro Glu Asn Ile Asn Phe Pro Ala Glu Glu Glu  
1 5 10 15

Lys Ile Leu Glu Phe Trp Thr Glu Phe Asn Cys Phe Gln Glu Cys Leu  
20 25 30

Lys Gln Ser Lys His Lys Pro Lys Phe Thr Phe Tyr Asp Gly Pro Pro  
35 40 45

Phe Ala Thr Gly Leu Pro His Tyr Gly His Ile Leu Ala Gly Thr Ile  
50 55 60



Gly	Arg	Leu	Leu	Val	Ala	Thr	Thr	Phe	Thr	His	Ser	Tyr	Pro	Phe	Cys	385	390	395	400
Trp	Arg	Ser	Asp	Thr	Pro	Leu	Ile	Tyr	Lys	Ala	Val	Pro	Ser	Trp	Phe	405	410	415	
Val	Arg	Val	Glu	Asn	Met	Val	Asp	Gln	Leu	Leu	Arg	Asn	Asn	Asp	Leu	420	425	430	
Cys	Tyr	Trp	Val	Pro	Glu	Leu	Val	Arg	Glu	Lys	Arg	Phe	Gly	Asn	Trp	435	440	445	
Leu	Lys	Asp	Ala	Arg	Asp	Trp	Thr	Ile	Ser	Arg	Asn	Arg	Tyr	Trp	Gly	450	455	460	
Thr	Pro	Ile	Pro	Leu	Trp	Val	Ser	Asp	Asp	Phe	Glu	Glu	Val	Val	Cys	465	470	475	480
Ile	Gly	Ser	Val	Ala	Glu	Leu	Glu	Glu	Leu	Ser	Gly	Ala	Lys	Ile	Ser	485	490	495	
Asp	Leu	His	Arg	Glu	Ser	Val	Asp	His	Leu	Thr	Ile	Pro	Ser	Arg	Cys	500	505	510	
Gly	Lys	Gly	Ser	Leu	His	Arg	Ile	Ser	Glu	Val	Phe	Asp	Cys	Trp	Phe	515	520	525	
Glu	Ser	Gly	Ser	Met	Pro	Tyr	Ala	Gln	Val	His	Tyr	Pro	Phe	Glu	Asn	530	535	540	
Lys	Arg	Glu	Phe	Glu	Asp	Ala	Phe	Pro	Ala	Asp	Phe	Ile	Ala	Glu	Gly	545	550	555	560
Ile	Asp	Gln	Thr	Arg	Gly	Trp	Phe	Tyr	Thr	Leu	Leu	Val	Leu	Ala	Thr	565	570	575	
Ala	Leu	Phe	Gly	Gln	Pro	Pro	Phe	Lys	Asn	Val	Ile	Val	Asn	Gly	Leu	580	585	590	
Val	Leu	Ala	Ser	Asp	Gly	Gln	Lys	Met	Ser	Lys	Arg	Lys	Lys	Asn	Tyr	595	600	605	
Pro	Asp	Pro	Val	Ser	Ile	Ile	Gln	Lys	Tyr	Gly	Ala	Asp	Ala	Leu	Arg	610	615	620	
Leu	Tyr	Leu	Ile	Asn	Ser	Pro	Val	Val	Arg	Ala	Glu	Asn	Leu	Arg	Phe	625	630	635	640
Lys	Glu	Glu	Gly	Val	Arg	Asp	Val	Leu	Lys	Asp	Val	Leu	Leu	Pro	Trp	645	650	655	
Tyr	Asn	Ala	Tyr	Arg	Phe	Leu	Ile	Gln	Asn	Val	Leu	Arg	Leu	Gln	Lys	660	665	670	
Glu	Glu	Glu	Ile	Glu	Phe	Leu	Tyr	Asn	Glu	Asn	Thr	Val	Arg	Glu	Ser	675	680	685	
Pro	Asn	Ile	Thr	Asp	Arg	Trp	Ile	Leu	Ser	Phe	Met	Gln	Ser	Leu	Ile	690	695	700	





Lys Gln Lys Glu Glu Glu Lys Arg Arg Lys Asp Glu Glu Lys Ala Glu  
 50 55 60  
 Lys Ala Lys Gln Ala Pro Lys Ala Ser Ser Gln Lys Ala Val Ala Ala  
 65 70 75 80  
 Asp Asp Glu Glu Met Asp Ala Thr Gln Tyr Tyr Glu Asn Arg Leu Lys  
 85 90 95  
 Tyr Leu Ala Ala Glu Lys Ala Lys Gly Glu Asn Pro Tyr Pro His Lys  
 100 105 110  
 Phe Ala Val Ser Met Ser Ile Pro Lys Tyr Ile Glu Thr Tyr Gly Ser  
 115 120 125  
 Leu Asn Asn Gly Asp His Val Glu Asn Ala Glu Glu Ser Leu Ala Gly  
 130 135 140  
 Arg Ile Met Ser Lys Arg Ser Ser Ser Ser Lys Leu Phe Phe Tyr Asp  
 145 150 155 160  
 Leu His Gly Asp Asp Phe Lys Val Gln Val Met Ala Asp Ala Ser Lys  
 165 170 175  
 Ser Gly Leu Asp Glu Ala Glu Phe Leu Lys Leu His Ser Asn Ala Lys  
 180 185 190  
 Arg Gly Asp Ile Val Gly Val Ile Gly Phe Pro Gly Lys Thr Lys Arg  
 195 200 205  
 Gly Glu Leu Ser Ile Phe Pro Arg Ser Phe Ile Leu Leu Ser His Cys  
 210 215 220  
 Leu His Met Met Pro Arg Lys Ala Asp Asn Val Asn Ala Lys Lys Pro  
 225 230 235 240  
 Glu Ile Trp Val Pro Gly Gln Thr Arg Asn Pro Glu Ala Tyr Val Leu  
 245 250 255  
 Lys Asp Gln Glu Ser Arg Tyr Arg Gln Arg His Leu Asp Met Ile Leu  
 260 265 270  
 Asn Val Glu Val Arg Gln Ile Phe Arg Thr Arg Ala Lys Ile Ile Ser  
 275 280 285  
 Tyr Val Arg Arg Phe Leu Asp Asn Lys Asn Phe Leu Glu Val Glu Thr  
 290 295 300  
 Pro Met Met Asn Met Ile Ala Gly Gly Ala Ala Ala Arg Pro Phe Val  
 305 310 315 320  
 Thr His His Asn Asp Leu Asp Met Arg Leu Tyr Met Arg Ile Ala Pro  
 325 330 335  
 Glu Leu Tyr Leu Lys Gln Leu Ile Val Gly Gly Leu Glu Arg Val Tyr  
 340 345 350  
 Glu Ile Gly Lys Gln Phe Arg Asn Glu Gly Ile Asp Leu Thr His Asn  
 355 360 365



Val Ser Lys Ala Ser His Ile Ser Arg Gly His Gln His Gln Ala Trp  
20 25 30

Gly Ser Arg Pro Pro Ala Ala Glu Cys Ala Thr Gln Arg Ala Pro Gly  
35 40 45

Ser Val Val Glu Leu Leu Gly Lys Ser Tyr Pro Gln Asp Asp His Ser  
50 55 60

Asn Leu Thr Arg Lys Val Leu Thr Arg Val Gly Arg Asn Leu His Asn  
65 70 75 80

Gln Gln His His Pro Leu Trp Leu Ile Lys Glu Arg Val Lys Glu His  
85 90 95

Phe Tyr Lys Gln Tyr Val Gly Arg Phe Gly Thr Pro Leu Phe Ser Val  
100 105 110

Tyr Asp Asn Leu Ser Pro Val Val Thr Thr Trp Gln Asn Phe Asp Ser  
115 120 125

Leu Leu Ile Pro Ala Asp His Pro Ser Arg Lys Lys Gly Asp Asn Tyr  
130 135 140

Tyr Leu Asn Arg Thr His Met Leu Arg Ala His Thr Ser Ala His Gln  
145 150 155 160

Trp Asp Leu Leu His Ala Gly Leu Asp Ala Phe Leu Val Val Gly Asp  
165 170 175

Val Tyr Arg Arg Asp Gln Ile Asp Ser Gln His Tyr Pro Ile Phe His  
180 185 190

Gln Leu Glu Ala Val Arg Leu Phe Ser Lys His Glu Leu Phe Ala Gly  
195 200 205

Ile Lys Asp Gly Glu Ser Leu Gln Leu Phe Glu Gln Ser Ser Arg Ser  
210 215 220

Ala His Lys Gln Glu Thr His Thr Met Glu Ala Val Lys Leu Val Glu  
225 230 235 240

Phe Asp Leu Lys Gln Thr Leu Thr Arg Leu Met Ala His Leu Phe Gly  
245 250 255

Asp Glu Leu Glu Ile Arg Trp Val Asp Cys Tyr Phe Pro Phe Thr His  
260 265 270

Pro Ser Phe Glu Met Glu Ile Asn Phe His Gly Glu Trp Leu Glu Val  
275 280 285

Leu Gly Cys Gly Val Met Glu Gln Gln Leu Val Asn Ser Ala Gly Ala  
290 295 300

Gln Asp Arg Ile Gly Trp Ala Phe Gly Leu Gly Leu Glu Arg Leu Ala  
305 310 315 320

Met Ile Leu Tyr Asp Ile Pro Asp Ile Arg Leu Phe Trp Cys Glu Asp  
325 330 335



Glu Arg Phe Leu Lys Gln Phe Cys Val Ser Asn Ile Asn Gln Lys Val  
340 345 350

Lys Phe Gln Pro Leu Ser Lys Tyr Pro Ala Val Ile Asn Asp Ile Ser  
355 360 365

Phe Trp Leu Pro Ser Glu Asn Tyr Ala Glu Asn Asp Phe Tyr Asp Leu  
370 375 380

Val Arg Thr Ile Gly Gly Asp Leu Val Glu Lys Val Asp Leu Ile Asp  
385 390 395 400

Lys Phe Val His Pro Lys Thr His Lys Thr Ser His Cys Tyr Arg Ile  
405 410 415

Thr Tyr Arg His Met Glu Arg Thr Leu Ser Gln Arg Glu Val Arg His  
420 425 430

Ile His Gln Ala Leu Gln Glu Ala Ala Val Gln Leu Leu Gly Val Glu  
435 440 445

Gly Arg Phe  
450

<210> 36

<211> 503

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 36

Met Ser Asp Phe Gln Leu Glu Ile Leu Lys Lys Leu Asp Glu Leu Asp  
1 5 10 15

Glu Ile Lys Ser Thr Leu Ala Thr Phe Pro Gln His Gly Ser Gln Asp  
20 25 30

Val Leu Ser Ala Leu Asn Ser Leu Lys Ala His Asn Lys Leu Glu Phe  
35 40 45

Ser Lys Val Asp Thr Val Thr Tyr Asp Leu Thr Lys Glu Gly Ala Gln  
50 55 60

Ile Leu Asn Glu Gly Ser Tyr Glu Ile Lys Leu Val Lys Leu Ile Gln  
65 70 75 80

Glu Leu Gly Gln Leu Gln Ile Lys Asp Val Met Ser Lys Leu Gly Pro  
85 90 95

Gln Val Gly Lys Val Gly Gln Ala Arg Ala Phe Lys Asn Gly Trp Ile  
100 105 110

Ala Lys Asn Ala Ser Asn Glu Leu Glu Leu Ser Ala Lys Leu Gln Asn  
115 120 125

Thr Asp Leu Asn Glu Leu Thr Asp Glu Thr Gln Ser Ile Leu Ala Gln  
130 135 140

Ile Lys Asn Asn Ser His Leu Asp Ser Ile Asp Ala Lys Ile Leu Asn  
145 150 155 160

Asp Leu Lys Lys Arg Lys Leu Ile Ala Gln Gly Lys Ile Thr Asp Phe  
165 170 175

Ser Val Thr Lys Gly Pro Glu Phe Ser Thr Asp Leu Thr Lys Leu Glu  
180 185 190

Thr Asp Leu Thr Ser Asp Met Val Ser Thr Asn Ala Tyr Lys Asp Leu  
195 200 205

Lys Phe Lys Pro Tyr Asn Phe Asn Ser Gln Gly Val Gln Ile Ser Ser  
210 215 220

Gly Ala Leu His Pro Leu Asn Lys Val Arg Glu Glu Phe Arg Gln Ile  
225 230 235 240

Phe Phe Ser Met Gly Phe Thr Glu Met Pro Ser Asn Gln Tyr Val Glu  
245 250 255

Thr Gly Phe Trp Asn Phe Asp Ala Leu Tyr Val Pro Gln Gln His Pro  
260 265 270

Ala Arg Asp Leu Gln Asp Thr Phe Tyr Ile Lys Asp Pro Leu Thr Ala  
275 280 285

Glu Leu Pro Asp Asp Lys Thr Tyr Met Asp Asn Ile Lys Ala Val His  
290 295 300

Glu Gln Gly Arg Phe Gly Ser Ile Gly Tyr Arg Tyr Asn Trp Lys Pro  
305 310 315 320

Glu Glu Cys Gln Lys Leu Val Leu Arg Thr His Ser Thr Ala Ile Ser  
325 330 335

Ala Arg Met Leu His Asp Leu Ala Lys Asp Pro Lys Pro Thr Arg Leu  
340 345 350

Phe Ser Ile Asp Arg Val Phe Arg Asn Glu Ala Val Asp Ala Thr His  
355 360 365

Leu Ala Glu Phe His Gln Val Glu Gly Val Leu Ala Asp Tyr Asn Ile  
370 375 380

Thr Leu Gly Asp Leu Ile Lys Phe Met Glu Glu Phe Phe Glu Arg Met  
385 390 395 400

Gly Val Thr Gly Leu Arg Phe Lys Pro Thr Tyr Asn Pro Tyr Thr Glu  
405 410 415

Pro Ser Met Glu Ile Phe Ser Trp His Glu Gly Leu Gln Lys Trp Val  
420 425 430

Glu Ile Gly Asn Ser Gly Met Phe Arg Pro Glu Met Leu Glu Ser Met  
435 440 445

Gly Leu Pro Lys Asp Leu Arg Val Leu Gly Trp Gly Leu Ser Leu Glu  
450 455 460

Arg Pro Thr Met Ile Lys Tyr Lys Val Gln Asn Ile Arg Glu Leu Leu  
465 470 475 480

Gly His Lys Val Ser Leu Asp Phe Ile Glu Thr Asn Pro Ala Ala Arg  
 485 490 495

Leu Asp Glu Asp Leu Tyr Glu  
 500

<210> 37  
 <211> 1440  
 <212> PRT  
 <213> Homo sapiens

<400> 37  
 Met Glu His Thr Glu Ile Asp His Trp Leu Glu Phe Ser Ala Thr Lys  
 1 5 10 15

Leu Ser Ser Cys Asp Ser Phe Thr Ser Thr Ile Asn Glu Leu Asn His  
 20 25 30

Cys Leu Ser Leu Arg Thr Tyr Leu Val Gly Asn Ser Leu Ser Leu Ala  
 35 40 45

Asp Leu Cys Val Trp Ala Thr Leu Lys Gly Asn Ala Ala Trp Gln Glu  
 50 55 60

Gln Leu Lys Gln Lys Lys Ala Pro Val His Val Lys Arg Trp Phe Gly  
 65 70 75 80

Phe Leu Glu Ala Gln Gln Ala Phe Gln Ser Val Gly Thr Lys Trp Asp  
 85 90 95

Val Ser Thr Thr Lys Ala Arg Val Ala Pro Glu Lys Lys Gln Asp Val  
 100 105 110

Gly Lys Phe Val Glu Leu Pro Gly Ala Glu Met Gly Lys Val Thr Val  
 115 120 125

Arg Phe Pro Pro Glu Ala Ser Gly Tyr Leu His Ile Gly His Ala Lys  
 130 135 140

Ala Ala Leu Leu Asn Gln His Tyr Gln Val Asn Phe Lys Gly Lys Leu  
 145 150 155 160

Ile Met Arg Phe Asp Asp Thr Asn Pro Glu Lys Glu Lys Glu Asp Phe  
 165 170 175

Glu Lys Val Ile Leu Glu Asp Val Ala Met Leu His Ile Lys Pro Asp  
 180 185 190

Gln Phe Thr Tyr Thr Ser Asp His Phe Glu Thr Ile Met Lys Tyr Ala  
 195 200 205

Glu Lys Leu Ile Gln Glu Gly Lys Ala Tyr Val Asp Asp Thr Pro Ala  
 210 215 220

Glu Gln Met Lys Ala Glu Arg Glu Gln Arg Ile Glu Ser Lys His Arg  
 225 230 235 240

Lys Asn Pro Ile Glu Lys Asn Leu Gln Met Trp Glu Glu Met Lys Lys  
 245 250 255

Gly	Ser	Gln	Phe	Gly	His	Ser	Cys	Cys	Leu	Arg	Ala	Lys	Ile	Asp	Met	260	265	270
Ser	Ser	Asn	Asn	Gly	Cys	Met	Arg	Asp	Pro	Thr	Leu	Tyr	Arg	Cys	Lys	275	280	285
Ile	Gln	Pro	His	Pro	Arg	Thr	Gly	Asn	Lys	Tyr	Asn	Val	Tyr	Pro	Thr	290	295	300
Tyr	Asp	Phe	Ala	Cys	Pro	Ile	Val	Asp	Ser	Ile	Glu	Gly	Val	Thr	His	305	310	315
Ala	Leu	Arg	Thr	Thr	Glu	Tyr	His	Asp	Arg	Asp	Glu	Gln	Phe	Tyr	Trp	325	330	335
Ile	Ile	Glu	Ala	Leu	Gly	Ile	Arg	Lys	Pro	Tyr	Ile	Trp	Glu	Tyr	Ser	340	345	350
Arg	Leu	Asn	Leu	Asn	Asn	Thr	Val	Leu	Ser	Lys	Arg	Lys	Leu	Thr	Trp	355	360	365
Phe	Val	Asn	Glu	Gly	Leu	Val	Asp	Gly	Trp	Asp	Asp	Pro	Arg	Phe	Pro	370	375	380
Thr	Val	Arg	Gly	Val	Leu	Arg	Arg	Gly	Met	Thr	Val	Glu	Gly	Leu	Lys	385	390	395
Gln	Phe	Ile	Ala	Ala	Gln	Gly	Ser	Ser	Arg	Ser	Val	Val	Asn	Met	Glu	405	410	415
Trp	Asp	Lys	Ile	Trp	Ala	Phe	Asn	Lys	Lys	Val	Ile	Asp	Pro	Val	Ala	420	425	430
Pro	Arg	Tyr	Val	Ala	Leu	Leu	Lys	Lys	Glu	Val	Ile	Pro	Val	Asn	Val	435	440	445
Pro	Glu	Ala	Gln	Glu	Glu	Met	Lys	Glu	Val	Ala	Lys	His	Pro	Lys	Asn	450	455	460
Pro	Glu	Val	Gly	Leu	Lys	Pro	Val	Trp	Tyr	Ser	Pro	Lys	Val	Phe	Ile	465	470	475
Glu	Gly	Ala	Asp	Ala	Glu	Thr	Phe	Ser	Glu	Gly	Glu	Met	Val	Thr	Phe	485	490	495
Ile	Asn	Trp	Gly	Asn	Leu	Asn	Ile	Thr	Lys	Ile	His	Lys	Asn	Ala	Asp	500	505	510
Gly	Lys	Ile	Ile	Ser	Leu	Asp	Ala	Lys	Phe	Asn	Leu	Glu	Asn	Lys	Asp	515	520	525
Tyr	Lys	Lys	Thr	Thr	Lys	Val	Thr	Trp	Leu	Ala	Glu	Thr	Thr	His	Ala	530	535	540
Leu	Pro	Ile	Pro	Val	Ile	Cys	Val	Thr	Tyr	Glu	His	Leu	Ile	Thr	Lys	545	550	555
Pro	Val	Leu	Gly	Lys	Asp	Glu	Asp	Phe	Lys	Gln	Tyr	Val	Asn	Lys	Asn	565	570	575

Ser	Lys	His	Glu	Glu	Leu	Met	Leu	Gly	Asp	Pro	Cys	Leu	Lys	Asp	Leu	580	585	590	
Lys	Lys	Gly	Asp	Ile	Ile	Gln	Leu	Gln	Arg	Arg	Gly	Phe	Phe	Ile	Cys	595	600	605	
Asp	Gln	Pro	Tyr	Glu	Pro	Val	Ser	Pro	Tyr	Ser	Cys	Lys	Glu	Ala	Pro	610	615	620	
Cys	Val	Leu	Ile	Tyr	Ile	Pro	Asp	Gly	His	Thr	Lys	Glu	Met	Pro	Thr	625	630	635	640
Ser	Gly	Ser	Lys	Glu	Lys	Thr	Lys	Val	Glu	Ala	Thr	Lys	Asn	Glu	Thr	645	650	655	
Ser	Ala	Pro	Phe	Lys	Glu	Arg	Pro	Thr	Pro	Ser	Leu	Asn	Asn	Asn	Cys	660	665	670	
Thr	Thr	Ser	Glu	Asp	Ser	Leu	Val	Leu	Tyr	Asn	Arg	Val	Ala	Val	Gln	675	680	685	
Gly	Asp	Val	Val	Arg	Glu	Leu	Lys	Ala	Lys	Lys	Ala	Pro	Lys	Glu	Asp	690	695	700	
Val	Asp	Ala	Ala	Val	Lys	Gln	Leu	Leu	Ser	Leu	Lys	Ala	Glu	Tyr	Lys	705	710	715	720
Glu	Lys	Thr	Gly	Gln	Glu	Tyr	Lys	Pro	Gly	Asn	Pro	Pro	Ala	Glu	Ile	725	730	735	
Gly	Gln	Asn	Ile	Ser	Ser	Asn	Ser	Ser	Ala	Ser	Ile	Leu	Glu	Ser	Lys	740	745	750	
Ser	Leu	Tyr	Asp	Glu	Val	Ala	Ala	Gln	Gly	Glu	Val	Val	Arg	Lys	Leu	755	760	765	
Lys	Ala	Glu	Lys	Ser	Pro	Lys	Ala	Lys	Ile	Asn	Glu	Ala	Val	Glu	Cys	770	775	780	
Leu	Leu	Ser	Leu	Lys	Ala	Gln	Tyr	Lys	Glu	Lys	Thr	Gly	Lys	Glu	Tyr	785	790	795	800
Ile	Pro	Gly	Gln	Pro	Pro	Leu	Ser	Gln	Ser	Ser	Asp	Ser	Ser	Pro	Thr	805	810	815	
Arg	Asn	Ser	Glu	Pro	Ala	Gly	Leu	Glu	Thr	Pro	Glu	Ala	Lys	Val	Leu	820	825	830	
Phe	Asp	Lys	Val	Ala	Ser	Gln	Gly	Glu	Val	Val	Arg	Lys	Leu	Lys	Thr	835	840	845	
Glu	Lys	Ala	Pro	Lys	Asp	Gln	Val	Asp	Ile	Ala	Val	Gln	Glu	Leu	Leu	850	855	860	
Gln	Leu	Lys	Ala	Gln	Tyr	Lys	Ser	Leu	Ile	Gly	Val	Glu	Tyr	Lys	Pro	865	870	875	880
Val	Ser	Ala	Thr	Gly	Ala	Glu	Asp	Lys	Asp	Lys	Lys	Lys	Lys	Glu	Lys	885	890	895	

Glu Asn Lys Ser Glu Lys Gln Asn Lys Pro Gln Lys Gln Asn Asp Gly	900	905	910
Gln Arg Lys Asp Pro Ser Lys Asn Gln Gly Gly Gly Leu Ser Ser Ser	915	920	925
Gly Ala Gly Glu Gly Gln Gly Pro Lys Lys Gln Thr Arg Leu Gly Leu	930	935	940
Glu Ala Lys Lys Glu Glu Asn Leu Ala Asp Trp Tyr Ser Gln Val Ile	945	950	955
Thr Lys Ser Glu Met Ile Glu Tyr His Asp Ile Ser Gly Cys Tyr Ile	965	970	975
Leu Arg Pro Trp Ala Tyr Ala Ile Trp Glu Ala Ile Lys Asp Phe Phe	980	985	990
Asp Ala Glu Ile Lys Lys Leu Gly Val Glu Asn Cys Tyr Phe Pro Met	995	1000	1005
Phe Val Ser Gln Ser Ala Leu Glu Lys Glu Lys Thr His Val Ala Asp	1010	1015	1020
Phe Ala Pro Glu Val Ala Trp Val Thr Arg Ser Gly Lys Thr Glu Leu	1025	1030	1035
Ala Glu Pro Ile Ala Ile Arg Pro Thr Ser Glu Thr Val Met Tyr Pro	1045	1050	1055
Ala Tyr Ala Lys Trp Val Gln Ser His Arg Asp Leu Pro Ile Lys Leu	1060	1065	1070
Asn Gln Trp Cys Asn Val Val Arg Trp Glu Phe Lys His Pro Gln Pro	1075	1080	1085
Phe Leu Arg Thr Arg Glu Phe Leu Trp Gln Glu Gly His Ser Ala Phe	1090	1095	1100
Ala Thr Met Glu Glu Ala Ala Glu Glu Val Leu Gln Ile Leu Asp Leu	1105	1110	1115
Tyr Ala Gln Val Tyr Glu Glu Leu Leu Ala Ile Pro Val Val Lys Gly	1125	1130	1135
Arg Lys Thr Glu Lys Glu Lys Phe Ala Gly Gly Asp Tyr Thr Thr Thr	1140	1145	1150
Ile Glu Ala Phe Ile Ser Ala Ser Gly Arg Ala Ile Gln Gly Gly Thr	1155	1160	1165
Ser His His Leu Gly Gln Asn Phe Ser Lys Met Phe Glu Ile Val Phe	1170	1175	1180
Glu Asp Pro Lys Ile Pro Gly Glu Lys Gln Phe Ala Tyr Gln Asn Ser	1185	1190	1195
Trp Gly Leu Thr Thr Arg Thr Ile Gly Val Met Thr Met Val His Gly	1205	1210	1215

Asp Asn Met Gly Leu Val Leu Pro Pro Arg Val Ala Cys Val Gln Val  
 1220 1225 1230  
 Val Ile Ile Pro Cys Gly Ile Thr Asn Ala Leu Ser Glu Glu Asp Lys  
 1235 1240 1245  
 Glu Ala Leu Ile Ala Lys Cys Asn Asp Tyr Arg Arg Arg Leu Leu Ser  
 1250 1255 1260  
 Val Asn Ile Arg Val Arg Ala Asp Leu Arg Asp Asn Tyr Ser Pro Gly  
 1265 1270 1275 1280  
 Trp Lys Phe Asn His Trp Glu Leu Lys Gly Val Pro Ile Arg Leu Glu  
 1285 1290 1295  
 Val Gly Pro Arg Asp Met Lys Ser Cys Gln Phe Val Ala Val Arg Arg  
 1300 1305 1310  
 Asp Thr Gly Glu Lys Leu Thr Val Ala Glu Asn Glu Ala Glu Thr Lys  
 1315 1320 1325  
 Leu Gln Ala Ile Leu Glu Asp Ile Gln Val Thr Leu Phe Thr Arg Ala  
 1330 1335 1340  
 Ser Glu Asp Leu Lys Thr His Met Val Val Ala Asn Thr Met Glu Asp  
 1345 1350 1355 1360  
 Phe Gln Lys Ile Leu Asp Ser Gly Lys Ile Val Gln Ile Pro Phe Cys  
 1365 1370 1375  
 Gly Glu Ile Asp Cys Glu Asp Trp Ile Lys Lys Thr Thr Ala Arg Asp  
 1380 1385 1390  
 Gln Asp Leu Glu Pro Gly Ala Pro Ser Met Gly Ala Lys Ser Leu Cys  
 1395 1400 1405  
 Ile Pro Phe Lys Pro Leu Cys Glu Leu Gln Pro Gly Ala Lys Cys Val  
 1410 1415 1420  
 Cys Gly Lys Asn Pro Ala Lys Tyr Tyr Thr Leu Phe Gly Arg Ser Tyr  
 1425 1430 1435 1440